

FIG. 1

SEQ ID NO: 1 HUMAN RAGE PARTIAL CODING SEQUENCE GenBank/EMBL Accession
No. M91211

1 ggggcagccg gaacagcagt tggagcctgg gtgctggtcc tcagtctgtg gggggcagta
61 gtaggtgctc aaaacatcac agcccggatt ggcgagccac tggtgctgaa gtgaagggg
121 gcccccaaga aaccaccca gcggttgaa tggaaactga acacaggccg gacagaagct
181 tggaaagtcc tgtctccca gggaggaggc cctgggaca gtgtggctcg tgccttccc
241 aacggctccc tcttcttc ggctgctggg atccaggatg aggggatttt ccggtgcagg
301 gcaatgaaca ggaatggaaa ggagaccaag tccaactacc gattccgtgt ctaccagatt
361 cctgggaagc cagaaattgt agattctgcc tctgaactca cggctggtgt tccaataag
421 gtggggacat gtgtgtcaga gggaagctac cctgcaggga ctcttagctg gcacttggat
481 gggaagcccc tgggtcctaa tgagaaggga gtatctgtga aggaacagac caggagacac
541 cctgagacag ggctcttcac actgcagtcg gagctaattg tgacccagc ccggggagga
601 gatccccgtc ccacttctc ctgtagcttc agcccaggcc ttccccgaca ccgggccttg
661 cgcacagccc ccatccagcc ccgtgtctgg gagcctgtgc ctctggagga ggtccaattg
721 gtggtggagc cagaagggtg agcagtagct cctggtggaa ccgtaaccct gacctgtgaa
781 gtcctgtccc agccctctcc tcaaattcac tggatgaagg atggtgtgcc ctgtcccctt
841 cccccagcc ctgtgtgat cctccctgag atagggcctc aggaccaggg aacctacagc
901 tgtgtggcca ccattccag ccacgggccc caggaaagcc gtgctgtcag catcagcatc
961 atcgaaccag gcgaggaggg gccaaactga ggctctgtgg gaggatcagg gctgggaact
1021 ctagccctgg ccttggggat cctgggaggc ctggggacag ccgccctgct cattggggtc
1081 atcttgtggc aaaggcggca acgccgagga gaggagagga aggccccaga aaaccaggag
1141 gaagaggagg agcgtgcaga actgaatcag tcggaggaac ctgaggcagg cgagagtagt
1201 actggagggc ctgaggggc ccacagacag atcccatcca tcagctccct ttctttttc
1261 ccttgaactg ttctggcctc agaccaactc tctcctgtat aatctcttc ctgtataacc
1321 ccacttgcc aagctttct ctacaaccag agccccccac aatgatgatt aaacacctga
1381 cacatctgc a

FIG. 2A

| | | |
|---|------|------------------------------|
| atg gca gcc gga aca gca gtt gga gcc tgg gtg ctg gtc ctc agt ctg Met Ala Ala Gly Thr Ala Val Gly Ala Trp Val Leu Val Leu Ser Leu 1 5 10 15 | 48 | SEQ ID NO: 2 SEQ ID NO: 3 |
| tgg ggg gca gta gta ggt gct caa aac atc aca gcc cgg att ggc gag Trp Gly Ala Val Val Gly Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu 20 25 30 | 96 | |
| cca ctg gtg ctg aag tgt aag ggg gcc ccc aag aaa cca ccc cag cgg Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg 35 40 45 | 144 | |
| ctg gaa tgg aaa ctg aac aca ggc cgg aca gaa gct tgg aag gtc ctg Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu 50 55 60 | 192 | |
| tct ccc cag gga gga ggc ccc tgg gac agt gtg gct cgt gtc ctt ccc Ser Pro Gln Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro 65 70 75 80 | 240 | |
| aac ggc tcc ctc ttc ctt ccg gct gtc ggg atc cag gat gag ggg att Asn Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile 85 90 95 | 288 | |
| ttc cgg tgc cag gca atg aac agg aat gga aag gag acc aag tcc aac Phe Arg Cys Gln Ala Met Asn Arg Asn Gly Lys Glu Thr Lys Ser Asn 100 105 110 | 336 | |
| tac cga gtc cgt gtc tac cag att cct ggg aag cca gaa att gta gat Tyr Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp 115 120 125 | 384 | |
| tct gcc tct gaa ctc acg gct ggt gtt ccc aat aag gtg ggg aca tgt Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr Cys 130 135 140 | 432 | |
| gtg tca gag gga agc tac cct gca ggg act ctt agc tgg cac ttg gat Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp 145 150 155 160 | 480 | |
| ggg aag ccc ctg gtg cct aat gag aag gga gta tct gtg aag gaa cag Gly Lys Pro Leu Val Pro Asn Glu Lys Gly Val Ser Val Lys Glu Gln 165 170 175 | 528 | |
| acc agg aga cac cct gag aca ggg ctc ttc aca ctg cag tcg gag cta Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu Leu 180 185 190 | 576 | |
| atg gtg acc cca gcc cgg gga gga gat ccc cgt ccc acc ttc tcc tgt Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser Cys 195 200 205 | 624 | |
| agc ttc agc cca ggc ctt ccc cga cac cgg gcc ttg cgc aca gcc ccc Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala Pro 210 215 220 | 672 | |
| atc cag ccc cgt gtc tgg gag cct gtg cct ctg gag gag gtc caa ttg Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln Leu 225 230 235 240 | 720 | |
| gtg gtg gag cca gaa ggt gga gca gta gct cct ggt gga acc gta acc Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val Thr 245 250 255 | 768 | |
| ctg acc tgt gaa gtc cct gcc cag ccc tct cct caa atc cac tgg atg Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp Met 260 265 270 | 816 | |
| aag gat ggt gtg ccc ttg ccc ctt ccc ccc agc cct gtg ctg atc ctc Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile Leu 275 280 285 | 864 | |
| cct gag ata ggg cct cag gac cag gga acc tac agc tgt gtg gcc acc Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr 290 295 300 | 912 | |
| cat tcc agc cac ggg ccc cag gaa agc cgt gct gtc agc atc agc atc His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser Ile 305 310 315 320 | 960 | |
| atc gaa cca ggc gag gag ggg cca act gca ggc tct gtg gga gga tca Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly Ser 325 330 335 | 1008 | |
| ggg ctg gtc tag Gly Leu Val | 1020 | |

FIG. 2B

SEQ ID NO: 4 HUMAN RAGE V-DOMAIN

gctc aaaacatcac agcccgatt ggcgagccac tgggtgctgaa gtgtaagggg
gcccccaaga aaccaccca gcggctggaa tggaaactga acacaggccg gacagaagct
tggaaggctc tgtctccca gggaggaggc ccctgggaca gtgtggctcg tgccttccc
aacggctccc tctcctcc ggctgtcggg atccaggatg aggggatttt ccggtgcagg
gcaatgaaca ggaatggaaa ggagaccaag tccaactacc gagtccgtgt ctaccagatt
cctgggaagc cagaaattgt agattctgcc tctgaactca cg

FIG. 2C

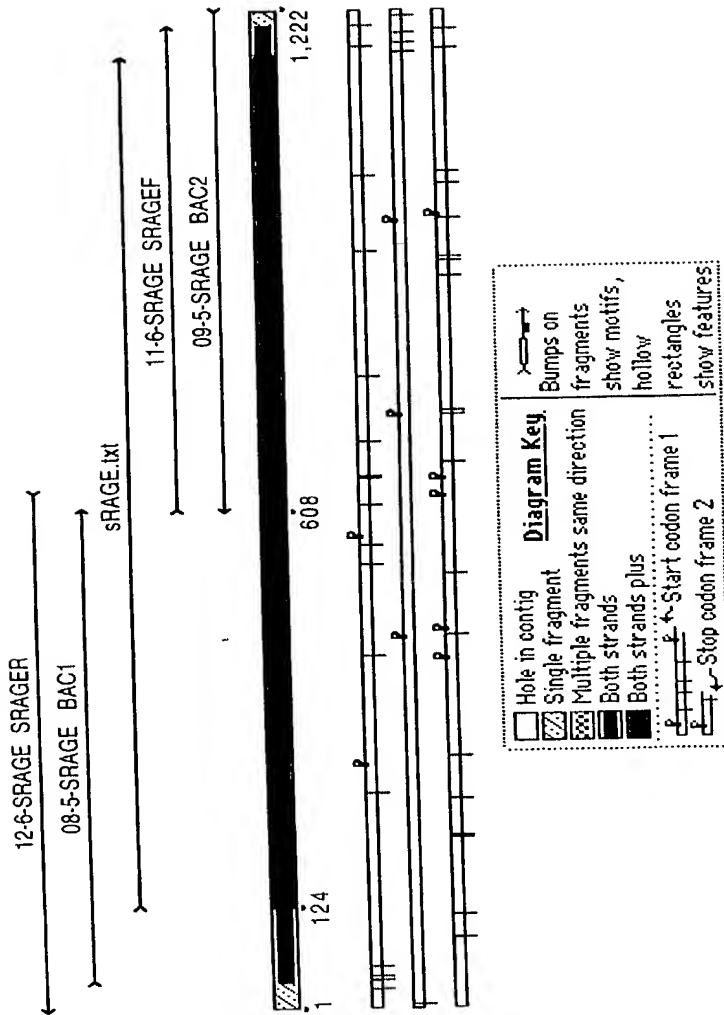


Fig. 3

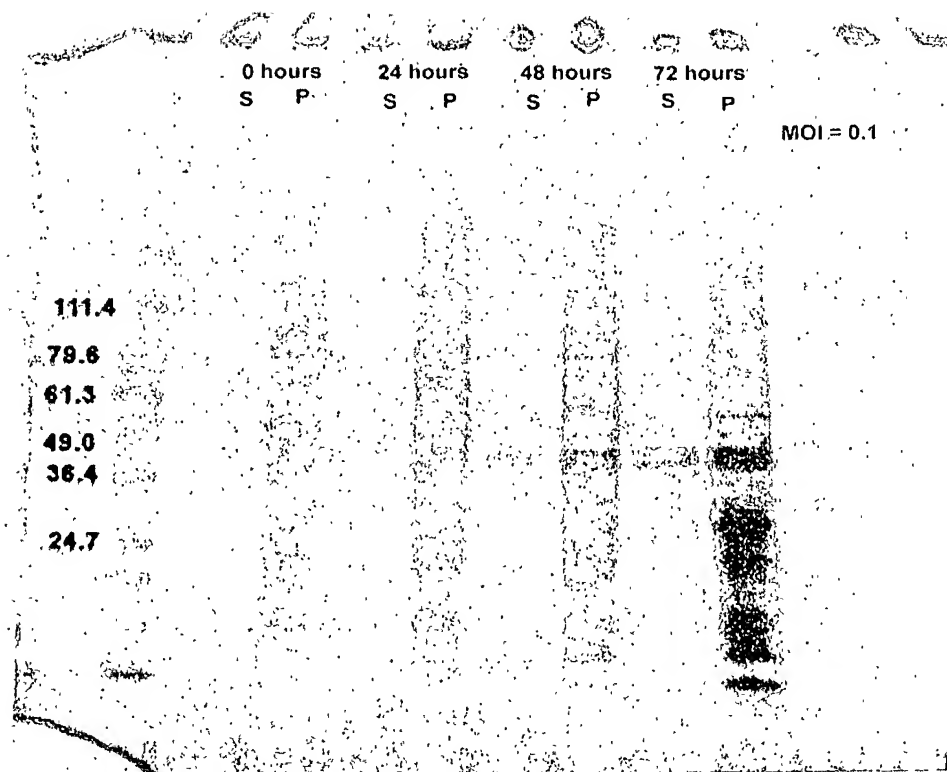


FIG. 4